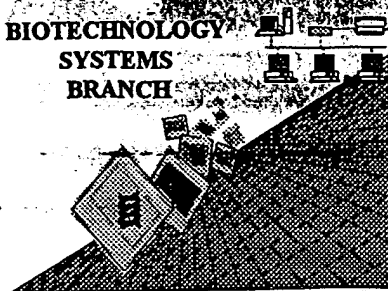


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/323,597A

Source: 1642

Date Processed by STIC: 9/11/2000

RECEIVED

SEP 18 2000

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/323,597A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

SEP 18 2000

TECH CENTER 1600/2900

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1642

RAW SEQUENCE LISTING DATE: 09/11/2000
 PATENT APPLICATION: US/09/323,597A TIME: 09:07:15

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\09112000\I323597A.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Daniel E. Afar
 4 Rene S. Hubert
 5 Kahan Leong
 6 Arthur B. Raitano
 7 Douglas C. Saffran
 8 Stephen C. Mitchell
 10 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
 11 AND THERAPY OF PROSTATE AND COLON CANCER
 14 <130> FILE REFERENCE: 129.8USU1
 16 <140> CURRENT APPLICATION NUMBER: 09/323,597A
 17 <141> CURRENT FILING DATE: 1999-06-01
 19 <150> PRIOR APPLICATION NUMBER: 60/087,598
 20 <151> PRIOR FILING DATE: 1998-06-01
 22 <150> PRIOR APPLICATION NUMBER: 60/091,474
 23 <151> PRIOR FILING DATE: 1998-06-29
 25 <150> PRIOR APPLICATION NUMBER: 60/129,521
 26 <151> PRIOR FILING DATE: 1999-04-14
 28 <160> NUMBER OF SEQ ID NOS: 13
 30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1738
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (112)...(1588)
 41 <400> SEQUENCE: 1
 42 ggcggaggcg gagcgagg ggcggggcg gggagcgccg cctggagcgc ggcaggtcat 60
 43 attgaacatt ccagatacct atcattactc gatgctgttg ataacagcaa g atg gct 117
 44 Met Ala
 45 1
 47 ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat 165
 48 Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
 49 5 10 15
 51 gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc 213
 52 Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
 53 20 25 30
 55 act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc 261
 56 Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
 57 35 40 45 50
 59 cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc 309
 60 Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys
 61 55 60 65
 63 acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag 357
 64 Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys
 65 70 75 80
 67 aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct 405

RAW SEQUENCE LISTING DATE: 09/11/2000
 PATENT APPLICATION: US/09/323,597A TIME: 09:07:15

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\09112000\I323597A.raw

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68 Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala
69      85      90      95
71 gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc      453
72 Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser
73      100      105      110
75 aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct      501
76 Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser
77 115      120      125      130
79 aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat      549
80 Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn
81      135      140      145
83 cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca      597
84 Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser
85      150      155      160
87 tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag      645
88 Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu
89      165      170      175
91 aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt      693
92 Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe
93      180      185      190
95 tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt atg      741
96 Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met
97 195      200      205      210
99 aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac      789
100 Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr
101      215      220      225
103 cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata      837
104 His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile
105      230      235      240
107 gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc      885
108 Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly
109      245      250      255
111 ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac      933
112 Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His
113      260      265      270
115 gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg      981
116 Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp
117 275      280      285      290
119 atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg      1029
120 Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp
121      295      300      305
123 cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat      1077
124 His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr
125      310      315      320
127 gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac      1125
128 Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp
129      325      330      335
131 tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct      1173
132 Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro

```


RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/323,597A

DATE: 09/11/2000
 TIME: 09:07:15

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\09112000\I323597A.raw

```

194          100          105          110
195 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
196          115          120          125
197 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
198          130          135          140
199 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
200 145          150          155          160
201 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
202          165          170          175
203 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
204          180          185          190
205 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
206          195          200          205
207 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
208          210          215          220
209 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
210 225          230          235          240
211 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
212          245          250          255
213 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
214          260          265          270
215 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
216          275          280          285
217 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
218          290          295          300
219 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
220 305          310          315          320
221 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
222          325          330          335
223 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
224          340          345          350
225 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
226          355          360          365
227 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
228          370          375          380
229 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
230 385          390          395          400
231 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
232          405          410          415
233 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
234          420          425          430
235 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
236          435          440          445
237 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
238          450          455          460
239 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
240 465          470          475          480
241 Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
242          485          490

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RAW SEQUENCE LISTING DATE: 09/11/2000
 PATENT APPLICATION: US/09/323,597A TIME: 09:07:15

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\09112000\I323597A.raw

```

244 <210> SEQ ID NO: 3
245 <211> LENGTH: 2479
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (57)...(1533)
253 <400> SEQUENCE: 3
254 gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac agcaag atg   59
255                                     Met
256                                     1
258 gct ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac   107
259 Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
260                                     5          10          15
262 cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc   155
263 His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
264                                     20          25          30
266 ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg   203
267 Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
268                                     35          40          45
270 ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc   251
271 Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
272 50          55          60          65
274 tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act   299
275 Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
276                                     70          75          80
278 aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga   347
279 Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
280                                     85          90          95
282 gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc   395
283 Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys
284                                     100         105         110
286 tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc   443
287 Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro
288                                     115         120         125
290 tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag   491
291 Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu
292 130          135          140          145
294 aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac   539
295 Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr
296                                     150         155         160
298 tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac   587
299 Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn
300                                     165         170         175
302 gag aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat   635
303 Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn
304                                     180         185         190
306 ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt   683
307 Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe

```

<210> 5
 <211> 388
 <212> DNA
 <213> Homo Sapiens

See item 10 on Ena Summary Sheet

<400> 5
 gatcttctg ctgagtcctt tccaggggcc aattttggat gagcatggag ctgtcacctc 60
 tcagctgctg gatgacttga gatgaaaaag gagagacatg gaaagggaga cagccaggtg 120
 gcacctgcag cggctgccct ctggggccac ttggtagtgt cccagccta cctctccaca 180
 aggggatttt gctgatgggt tcttanagcc ttagcagccc tggatgggtg ccagaaataa 240
 agggaccagc ccttcatggg tggtgacgtg gtaattcactt gtaaggggaa cagaaacatt 300
 ttgtttctta tggggtgaga atatagacag tgcccttggg gcgaggggaag caattgaaaa 360
 ggaacttgcc ctgagcactc ctggtgca 388

VERIFICATION SUMMARY

DATE: 09/11/2000

PATENT APPLICATION: US/09/323,597A

TIME: 09:07:16

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\09112000\I323597A.raw

L:168 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 1
 L:379 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 3
 L:477 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
 L:477 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
 L:477 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:477 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
 L:477 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
 L:478 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
 L:478 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
 L:478 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:478 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
 M:340 Repeated in SeqNo=5